

| | |
|-----|--------------|
| 1: | em.estbna.* |
| 2: | em.estbna.* |
| 3: | em.estlin.* |
| 4: | em.estlmu.* |
| 5: | em.estmov.* |
| 6: | em.estpl.* |
| 7: | em.estro.* |
| 8: | em.htc.* |
| 9: | gd.est1.* |
| 10: | gd.est2.* |
| 11: | gd.htc.* |
| 12: | gd.est3.* |
| 13: | gd.est4.* |
| 14: | gd.est5.* |
| 15: | em.estfun.* |
| 16: | em.estom.* |
| 17: | em.gss_hum.* |
| 18: | em.gss_huv.* |
| 19: | em.gss_pln.* |
| 20: | em.gss_vrt.* |
| 21: | em.gss_fun.* |
| 22: | em.gss_hum.* |
| 23: | em.gss_mus.* |
| 24: | em.gss_pro.* |
| 25: | em.gss_rod.* |
| 26: | em.gss_phg.* |
| 27: | em.gss_vrt.* |
| 28: | gd.gss1.* |

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Description

| | | | | | | |
|----|-----|------|------|----|----------|----------|
| 1 | 286 | 81.7 | 1201 | 13 | BX46370 | BX46370 |
| 2 | 275 | 78.6 | 1201 | 9 | AL58197 | AL58197 |
| 3 | 267 | 76.3 | 857 | 13 | BH172435 | BH172435 |
| 4 | 267 | 76.3 | 930 | 13 | BX393871 | BX393871 |
| 5 | 256 | 73.1 | 836 | 13 | BQ228243 | BQ228243 |
| 6 | 243 | 69.4 | 957 | 9 | AL521920 | AL521920 |
| 7 | 242 | 69.1 | 1117 | 12 | BM545164 | BM545164 |
| 8 | 237 | 67.7 | 890 | 9 | AL520538 | AL520538 |
| 9 | 221 | 63.1 | 1019 | 12 | BM557530 | BM557530 |
| 10 | 216 | 61.7 | 1201 | 9 | AL529615 | AL529615 |
| 11 | 214 | 61.1 | 827 | 13 | BQ437698 | BQ437698 |
| 12 | 214 | 61.1 | 929 | 13 | BH853307 | BH853307 |
| 13 | 213 | 60.9 | 759 | 10 | BE275324 | BE275324 |
| 14 | 211 | 60.3 | 817 | 12 | BH755123 | BH755123 |
| 15 | 210 | 60.0 | 1201 | 13 | BX377118 | BX377118 |
| 16 | 208 | 59.4 | 843 | 13 | BH848893 | BH848893 |
| 17 | 208 | 59.4 | 980 | 13 | BH854847 | BH854847 |
| 18 | 203 | 58.0 | 963 | 10 | BE797115 | BE797115 |
| 19 | 202 | 57.7 | 859 | 10 | BE975933 | BE975933 |
| 20 | 201 | 57.4 | 945 | 10 | BE747311 | BE747311 |
| 21 | 198 | 56.6 | 958 | 10 | BF973889 | BF973889 |
| 22 | 197 | 56.3 | 845 | 10 | BG754550 | BG754550 |
| 23 | 194 | 55.4 | 728 | 14 | CD102399 | CD102399 |
| 24 | 189 | 54.0 | 568 | 14 | CB122465 | CB122465 |
| 25 | 189 | 54.0 | 732 | 10 | BG472953 | BG472953 |
| 26 | 189 | 54.0 | 1031 | 13 | BX385102 | BX385102 |
| 27 | 185 | 52.9 | 600 | 14 | CB145277 | CB145277 |
| 28 | 183 | 52.3 | 549 | 12 | BM71181 | BM71181 |
| 29 | 180 | 51.4 | 638 | 14 | CB122989 | CB122989 |
| 30 | 180 | 51.4 | 909 | 13 | BH165031 | BH165031 |
| 31 | 177 | 50.6 | 1074 | 10 | BX339176 | BX339176 |
| 32 | 177 | 50.6 | 1119 | 10 | BG745052 | BG745052 |
| 33 | 174 | 49.7 | 610 | 12 | BM841141 | BM841141 |
| 34 | 174 | 49.7 | 920 | 10 | BF696536 | BF696536 |
| 35 | 173 | 49.4 | 742 | 12 | BT093955 | BT093955 |
| 36 | 172 | 49.1 | 666 | 13 | BD663511 | BD663511 |
| 37 | 172 | 49.1 | 888 | 13 | BH195469 | BH195469 |
| 38 | 170 | 48.6 | 562 | 12 | BM842929 | BM842929 |
| 39 | 164 | 46.9 | 753 | 10 | BE727240 | BE727240 |
| 40 | 162 | 46.3 | 785 | 10 | AM957667 | AM957667 |
| 41 | 161 | 46.0 | 905 | 10 | BF973755 | BF973755 |
| 42 | 161 | 46.0 | 1032 | 12 | BM810545 | BM810545 |
| 43 | 161 | 46.0 | 1201 | 9 | AL582089 | AL582089 |
| 44 | 159 | 44.9 | 628 | 10 | BF034644 | BF034644 |
| 45 | 157 | 44.9 | 472 | 14 | CB142204 | CB142204 |
| | | | | | | |
| | | | | | BX46370 | BX46370 |
| | | | | | AL58197 | AL58197 |
| | | | | | BH172435 | BH172435 |
| | | | | | BX393871 | BX393871 |
| | | | | | BQ228243 | BQ228243 |
| | | | | | AL521920 | AL521920 |
| | | | | | BM545164 | BM545164 |
| | | | | | AL520538 | AL520538 |
| | | | | | BM557530 | BM557530 |
| | | | | | AL529615 | AL529615 |
| | | | | | BQ437698 | BQ437698 |
| | | | | | BH853307 | BH853307 |
| | | | | | BE275324 | BE275324 |
| | | | | | BH755123 | BH755123 |
| | | | | | BX377118 | BX377118 |
| | | | | | BH848893 | BH848893 |
| | | | | | AL520538 | AL520538 |
| | | | | | BE797115 | BE797115 |
| | | | | | BE975933 | BE975933 |
| | | | | | BE747311 | BE747311 |
| | | | | | BF973889 | BF973889 |
| | | | | | BG754550 | BG754550 |
| | | | | | CD102399 | CD102399 |
| | | | | | CB122465 | CB122465 |
| | | | | | BG472953 | BG472953 |
| | | | | | BX385102 | BX385102 |
| | | | | | CB145277 | CB145277 |
| | | | | | BM71181 | BM71181 |
| | | | | | CB122989 | CB122989 |
| | | | | | BH165031 | BH165031 |
| | | | | | BX339176 | BX339176 |
| | | | | | BG745052 | BG745052 |
| | | | | | BM841141 | BM841141 |
| | | | | | BF696536 | BF696536 |
| | | | | | BT093955 | BT093955 |
| | | | | | BD663511 | BD663511 |
| | | | | | BM842929 | BM842929 |
| | | | | | BE727240 | BE727240 |
| | | | | | AM957667 | AM957667 |
| | | | | | BF973755 | BF973755 |
| | | | | | BM810545 | BM810545 |
| | | | | | AL582089 | AL582089 |
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| | | | | | CB142204 | CB142204 |
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|------------|----------|--|------|--------|-----------------|
| LOCUS | BX446370 | 1201 bp | mRNA | linear | EST 22-MAY-2003 |
| DEFINITION | BX446370 | Homo sapiens PLACENTA Homo sapiens cDNA clone CL08A0042B11 | | | |

5-PRIME, mRNA sequence.

| | |
|-----------|-------------|
| ACCESSION | BX446370 |
| VERSION | BX446370.1 |
| | GI:31023721 |

| KEYWORDS | EST. |
|----------|----------------------|
| SOURCE | Homo sapiens (human) |

ORGANISM

REFERENCE
1 (bases 1 to 1201)

Db 303 CTGAATTGACTAGAGAGGCTTTGATGACGAGGTGTAGATTTTCTTCCCGGAACAAACA 362
QY 204 TleutrglnlystrhglnlleuSerleuGlnlySProleuLeuHnistrhglymet 223
363 CTTTATCAGAGAGAGAAATTCGTCTGACAGAGAGCTTTGGTCTTACATACGAGATG 422
QY 224 GtlyarlgucystrhglnleuSergluserValSerleuAlathrmetlleaspaglylely 243
423 GGAAGGTTATGACACACGATGATGTCTCTCCCTGCAACCAATGATGATCGAATGAAA 482
QY 244 ArgHistrleuSergHistrleuSergHistrleuSergHistrleuSergHistrleuSerg 263
483 AGACACTAAACATATCTATTCCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 542
QY 264 GlnVallyValValAlaleuGlnlySerglySerglySerglySerglySerglySergly 283
543 CAAGTCAAAAGTCCGCGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 602
QY 284 AlaspheutryleutrhnglyglumetSerHistrleuSphrleuSphrleuSphrleuSphr 303
603 GCTGACCTTAACTCAGAGGTGAGATGTCCCATCATATATCTTGTGATGCTGCTCCAA 662
QY 304 GtlyleasnVallleuGlnlySerglySerglySerglySerglySerglySerglySergly 323
663 GGAATTAATGATCATCTCTGTGAGACAGACAGACAGACAGACAGACAGACAGACAGAC 722
QY 324 ArgAspmetleuAspSerHistrleuGlnlySerglySerglySerglySerglySergly 343
723 CGAGATATGCTGTGATCTCACTTGTGAGATTAATATATATATATATATATATATATAT 782
QY 344 ArgAspProleuGlnlyVal 350
783 AGGAGCCCTCTTCAGGTGTGTA 803
Db

RESULT 4
BX393871 930 bp mRNA linear EST 13-MAY-2003
LOCUS BX393871 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DC0051M21 5-PRIME, mRNA sequence.
ACCESSION BX393871
VERSION BX393871.1 GI:30624084
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 930)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bld/cluster.cgi?seq=CS0DC005A10P1cluster=1287.f. Contact :
Peng liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/>
Paraday Avenue Genoscope sequence ID: CS0DC005A10P1.
location/Qualifiers
1..930
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC0051M21"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V

BASE COUNT 248 a 231 c 214 g 237 t sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 8,14e-249 Length: 930
Score: 267.00 Matches: 267
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 76.29% Indels: 0
DB: 13 Gaps: 0
US-09-745-506-37 (1-350) x BX393871 (1-930)
QY 1 MetAspLeuValAlaleuSerleuSphrleuSphrleuSphrleuSphrleuSphrleuSphr 20
Db 130 ATGATTTGAGAGGCT 189
QY 21 SerTrpAspAsnValGtlyleuLeuValGtlyleuSphrleuSphrleuSphrleuSphrleu 40
Db 190 AGTGGGACAAATGTTGGATTTACTGTGTGAACCAAGCCACACATCTGTAATACACTC 249
QY 41 PheLeuThrAsnAspLeuThrGlnGluValMetGlnGluValLeuGlnlySphrleuSphrleu 60
Db 250 TTCTTGACCAATGACCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 309
QY 61 LeuLeuSerlyrHnistrProleuPheArgProleuSphrleuSphrleuSphrleuSphrleu 80
Db 310 CTCAATCT 369
QY 81 TrpLysGlnArgleuVallleuArgAlaleuGlnlySphrleuSphrleuSphrleuSphrleu 100
Db 370 TGGAGAGAGCCCTGT 429
QY 101 ThrAlaTrpAspAlaAlaProGlnlyValAsnAsnTrpLeuAlaValSphrleuGlyleuGlyAla 120
Db 430 ACAGCGTATGATGTGCGGCCCGCCAGGCGCTCAACAACTGTGTGTGTGTGTGTGTGTGTGT 489
QY 121 CysThrSerArgProleuHnistrProleuSphrleuSphrleuSphrleuSphrleuSphr 140
Db 490 GTTACCTTCCAGGCCCATCATCT 549
QY 141 ArgValGlnPheAsnValAsnTrpTrpGlnAspLeuSphrleuSphrleuSphrleuSphrleu 160
Db 550 CGAGTAGAATTCACACGTTTAACTACACCAACCTGACCAAGTCATGTCTGCGAGTGA 609
QY 161 GtlyleaspGlyValSerValThrSerPheSerAlaArgTrhglnGlnGlnGlnGlnGln 180
Db 610 GGAATGTAGCGGT 669
QY 181 ArgIleAsnLeuAsnCysTrhglnlySphrleuSphrleuSphrleuSphrleuSphrleuSphr 200
Db 670 CGGATTAATTCGATTTGTACTACAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 729
QY 201 AsnlysglnleuTrhglnlySphrleuSphrleuSphrleuSphrleuSphrleuSphrleu 220
Db 730 AACCAACACCTTTTACAGAGAGGAAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 789
QY 221 ThrGlnMetGtlyarlgucystrhglnleuSphrleuSphrleuSphrleuSphrleuSphr 240
Db 790 ACTGGAATGGAGCGGTTTGTGACACTGTGATGATGTCTCTCTCTCTCTCTCTCTCTCTCT 849
QY 241 ArgIlelySargHistrleuSphrleuSphrleuSphrleuSphrleuSphrleuSphrleu 260
Db 850 CGAATTAATAAGACACCTTAATACTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 909
QY 261 LeuGlnuserGlnlyValVal 267
Db 910 TTAGAGTCTCAAGTCAAGTC 930
LOCUS BQ229243 836 bp mRNA linear EST 02-MAY-2002

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DEFINITION  AGENCOURT_7510797 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6055296
5', mRNA sequence.
ACCESSION   BQ229243
VERSION     BQ229243.1 GI:20410643
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 836)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgarbs-remail.nih.gov
            Tissue Procurement: ATCC/DCPD/OTF
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM13315 row: f column: 01
            High quality sequence stop: 677.
            Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6055296"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NCI;
                Site:2: Sall; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 2 kb. Library constructed by Life
                Technologies."
BASE COUNT   218 a 205 c 200 g 211 t 2 others
ORIGIN
Alignment Scores:
Pred. No.:      3,58e-238      length:      836
Score:          256.00         Matches:     256
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%   Mismatches:  0
Query Match:    73.14%         Indels:       0
DB:             13            Gaps:         0
US-09-745-506-37 (1-350) x BQ229243 (1-836)
QY      3 LeuUyAAlaLeuLeuSerSerLeuAnaAspPheAlaSerLeuSerPheAlaGluSerTrp 22
Db      2 TTGAAGGCTCTCTCTCTCTCTGAAATGAGCTTGCCTCCGTTGCTGAGAGTTGG 61
QY      23 AspAsnValGlyLeuLeuValGluProSerProPheHisThrValAsnThrLeuPheLeu 42
Db      62 GACATAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 121
QY      43 ThrAsnAspLeuThrGluGluValMetGluGluValLeuGluGluValLeuGluGlu 62
Db      122 ACCAATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 181
QY      63 LeuSerTrpHisProPheProIlePheArgPheMetLeuArgTrpIleThrTrpAsnThrTrp 82
Db      182 CTCTCTTACCATCCGCTATCTCTCCAGACCATGAAACCGATTAACCTGGAACATGGAAG 241
QY      83 GluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHisThrAla 102
Db      242 GAGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
QY      103 TyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaGlyGluGlyAlaGlyTrp 122
Db      302 TATGATGCTGCGCCCGGCGTCAACACACTGCTGCTAAAGGCGCTTGAGCTTGTACC 361

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QY      123 SerArgProIleHisProSerLysAlaProAsnTyrProThrGluGluAsnHisArgVal 142
Db      362 TCCAGGCCCATATCATCTCTCCAAAGCTCCCACTACCTACAGAGGAAACCCAGATA 421
QY      143 GluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValGlyGly 162
Db      422 GAATTCACAGTTATACATACACCCAGACCTGAGACAGTATGATGATGATGATGATGAT 481
QY      163 AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIle 182
Db      482 GAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 541
QY      183 AsnLeuAsnGlyThrGlnGluValAlaLeuMetGluValValAspPheLeuSerArgAsn 202
Db      542 AATCTTAATATGATCTCAAGAAAGGCTTGAAGCAGAGTGAATTTCTTCTCCGGAACAA 601
QY      203 GlnLeuTyrGlnLysThrGluLeuSerLeuGluLysProLeuLeuHisThrGly 222
Db      602 CAATTTATACAGAAAGCGGAATTTGTCACCTGAGAGAGCTTGGTCTACATACGAGA 661
QY      223 MetGlyArgLeuGlyThrLeuAspGluSerValSerLeuAlaThrMetLeuAspArgIle 242
Db      662 ATGGAGCGGTTATGACACACTGATGATGATGATGATGATGATGATGATGATGATGAT 721
QY      243 LysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGly 258
Db      722 AAAAGACCTTAATACATCTCATTTGCTTACCTTGAGCCCTTGAGGTGGGG 769
RESULT 6
AL521920 957 bp mRNA linear EST 22-MAY-2003
LOCUS     AL521920
DEFINITION Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
CDNA clone CS0DB003YPI4 5-PRIME, mRNA sequence.
ACCESSION AL521920
VERSION   AL521920.2 GI:31040194
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS   Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
COMMENT   On Feb 13, 2001 this sequence version replaced gi:12785413.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DB003YPI4
Feng Liang Email: fliang@life.technet.com; Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DB003YPI4.
Location/Qualifiers
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    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DB003YPI4"
    /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
    /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
    /note="1st strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with Not I and cloned into the Not I and EcoR V
    sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 250 a 239 c 217 g 250 t 1 others
ORIGIN

```

Alignment Scores:

Pred. No.: 1,79e-225 Length: 957
 Score: 243.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 69.43% Indels: 0
 DB: 9 Gaps: 0

US-09-745-506-37 (1-350) x AL521920 (1-957)

QY 1 MetaspLeuYsAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 DB 166 ATGGATTGGAAGGCTCCCTCTCTCTCTGATGACTTGTGATCCCTCTGCTGAG 225
 QY 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProPheAlaThrValAsnThrLeu 40
 DB 226 AGTTGGACAATGTGGATTACTGTGTGAACCAAGCCACCAACATGTAATACACTC 285
 QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
 DB 286 TTCTGTGACCAATGACCTGACTGAGAGATGATGAGAGATGTCACAAAGAGGACAC 345
 QY 61 LeuLeuSerSerTrpHisProPheArgPheArgProMetLysArgLleThrTrpAsnThr 80
 DB 346 CTCATTCTCTCTACCAATCCCTATCTTCGACCCATGAGCCCATTAACCTGGAACACA 405
 QY 81 TrpLysGluArgLeuValLleArgAlaLeuGlnAsnArgValGlyLleTrSerProHis 100
 DB 406 TGGAAAGAGCGCCGTGGATCCGGGCTGGAGAAAGAGTGGTATCTCTCTCTCAT 465
 QY 101 ThrAlaTrpAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
 DB 466 ACACCCATGATGATGTCGCGCCCGCCAGGCGTCACAACTGTGGCTTAAGGCGCTGGACT 525
 QY 121 CysThrSerArgProLleHisProSerLysAlaProAsnTrpProThrGluGlyAsnHis 140
 DB 526 TGTACCTCCAGCCCATATCATCTTCCAAAGCTCCCACTACCTACAGAGAGAAACAC 585
 QY 141 ArgValGluPheAsnValAsnTrpThrGlnAspLeuAspLysValMetSerAlaValLys 160
 DB 586 CGAGTAGAATTCACAGCTTACTACACCCAGACCTGGACAAAGTCATCTCTGCACTGAAA 645
 QY 161 GlyLleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluThr 180
 DB 646 GGAATGTGCGGTTGTTCTGTCATCTTCTTCTGCTAGACTGCTAATGAGAGACAAACA 705
 QY 181 ArgLleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
 DB 706 CGGATTAATCATGAAATGTACACAGAAAGCTTGTGATGCAAGTGTGATTTCTTCCCG 765
 QY 201 AsnLysGlnLeuTrpGlnLysThrGluLleLeuSerLeuGluLysProLeuLeuHis 220
 DB 766 AACCAAAACAACTTATACAGAGCGGAAATCTGTACACGAGAACCCCTTGTCTTCAAT 825
 QY 221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetLleAsp 240
 DB 826 ACTGGAATGGAGCGGTATGCACTGATGATATCTGTCTCTGCAACCATGATGAT 885
 QY 241 ArgLleLys 243
 DB 886 CGAATTAATA 894
 RESULT 7
 LOCUS BM545164 1117 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6497454 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588980
 ACCESSION BM545164
 VERSION BM545164
 KEYWORDS 5' mRNA sequence.
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1117)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Invitrogen
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM12360 row: p column: 05
 High quality sequence stop: 734.
 Location/Qualifiers

FEATURES

source 1. 1117

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5588980"
 /lab_host="DH10B"
 /clone_1lb="NIH_MGC_125"
 /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
 Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
 of three ovaries, from females ranging in age from 38 to
 49 yo. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 2.1 kb, insert size range 1-3.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 036."

BASE COUNT 278 a 282 c 260 g 293 t 4 others
 ORIGIN

Alignment Scores:

Pred. No.: 1.98e-224 Length: 1117
 Score: 242.00 Matches: 242
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 69.14% Indels: 0
 DB: 12 Gaps: 0

US-09-745-506-37 (1-350) x BM545164 (1-1117)

QY 1 MetaspLeuYsAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 DB 88 ATGGATTGGAAGGCTCCCTCTCTCTGATGACTTGTGATCCCTCTGCTGAG 147
 QY 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProPheAlaThrValAsnThrLeu 40
 DB 148 AGTTGGACAATGTGGATTACTGTGTGAACCAAGCCACCAATGTAATACACTC 207
 QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
 DB 208 TTCTGTGACCAATGACCTGAGAGATGATGAGAGATGTCACAAAGAGGACAGAC 267
 QY 61 LeuLeuSerSerTrpHisProPheArgPheArgProMetLysArgLleThrTrpAsnThr 80
 DB 268 CTCATTCTCTCTACCAATCCGCTATCTTCCAGACCAATGAGCGCATTAACCTGGAACACA 327
 QY 81 TrpLysGluArgLeuValLleArgAlaLeuGlnAsnArgValGlyLleTrSerProHis 100
 DB 328 TGGAAAGAGCGCGCTGTATCGGCTGTGGAGAACAGTGGTATCTACTCTCTCAT 387
 QY 101 ThrAlaTrpAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
 DB 388 ACAGCCTATGATGTCGCGCCCGCCAGGCGTCACAACTGATGCTTAAGGCGTTGAGACT 447
 QY 121 CysThrSerArgProLleHisProSerLysAlaProAsnTrpProThrGluGlyAsnHis 140
 DB 448 TGTACTCCAGGCCCATATCATCTTCCAAAGCTCCCACTACCTACAGAGAGAAACAC 507

QY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
 DB 508 CGAGTAGAATTCACAGTTACTACACACCAAGCTGCAAAAGTCTGTCAGAGTAA 567
 QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGlnThr 180
 DB 568 GCAATTGACGGTGTCT 627
 QY 181 ArgIleAsnLeuAsnGlyThrGlnLysAlaLeuMetGluValValAspPheLeuSerArg 200
 DB 628 CGGATTAACTCAATGTAAGTCAAGAGCGCTTGTGATGCAAGGTGATATTTCTCTCCG 687
 QY 201 AsnLysGlnLeuTyrGlnLysThrGlnLysLeuSerLeuGluLysProLeuLeuHis 220
 DB 688 AACAAACAATTATCAGAACAGCAAAATTCCTGCTCAGAGAGCTTGTCTTCTACT 747
 QY 221 ThrGlyMetGlyArgLeuGlyThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
 DB 748 ACTGGAATGGACGGTTATGACACACTGATGATGATGCTCTCCCTGCAACCATGATGAT 807
 QY 241 ArgIle 242
 DB 808 CGAATA 813
 RESULT 8
 AL520538 890 bp mRNA linear EST 22-MAY-2003
 LOCUS AL520538 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
 DEFINITION CDNA clone CS0DB006Y18 5-PRIME, mRNA sequence.
 ACCESSION AL520538
 VERSION AL520538.2 GI:31038879
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 890)
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 13, 2001 this sequence version replaced gi:12784031.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by life technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1287.f for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DB006DC090P1a;cluster=1287.f. Contact :
 Peng Liang Email: filiang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DB006DC090P1.
 FEATURES
 source
 1..890
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DB006Y18"
 /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-poly(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 230 a 224 c 201 g 234 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,12e-219 Length: 890
 Score: 237.00 Matches: 237
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 67.71% Indels: 0
 DB: 9 Gaps: 0
 US-09-745-506-37 (1-350) x AL520538 (1-890)
 QY 1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 DB 178 ATGAGTTAAGAGCT 237
 QY 21 SerTTPAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
 DB 238 AGTTGGACCAATGTTGATTAAGTCTGAGAACCAACCCACACATATCTGTAATACATC 297
 QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuLysLysAlaAsp 60
 DB 298 TTCCCTGACCAATGACCTGACTGAGGAAGATGAGAGAGTGTGAAAAAARAGGAGAC 357
 QY 61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTTPAsnThr 80
 DB 358 CTCATCT 417
 QY 81 TPlySGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
 DB 418 TGGAGAGACCGCTGTGATCCGGCTCTGAGAACAGAGTGGTATCTACTCTCTCTCAT 477
 QY 101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAspTTPLeuAlaLysGlyLeuGlyAla 120
 DB 478 ACAGCCTATGATGCTGCGCCCGCCGAGCAACACTGGTGTGCTAAAGGCTTGAGAGCT 537
 QY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
 DB 538 TGTACTCTCCAGGCCCTATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 597
 QY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
 DB 598 CGAGTAGAATTCACAGTTACTACACACCAAGCTGCAAAAGTCTGTCAGAGTAA 657
 QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGlnThr 180
 DB 658 GGAATGGACGGTGTCT 717
 QY 181 ArgIleAsnLeuAsnGlyThrGlnLysAlaLeuMetGluValValAspPheLeuSerArg 200
 DB 718 CGGATTAACTCAATGTAAGTCAAGAGCGCTTGTGATGCAAGGTGATATTTCTTCCCG 777
 QY 201 AsnLysGlnLeuTyrGlnLysThrGlnLysLeuSerLeuGluLysProLeuLeuHis 220
 DB 778 AACAAACAATTATCAGAACAGCAAAATTCCTGCTCAGAGAGCTTGTGCTTCTACT 837
 QY 221 ThrGlyMetGlyArgLeuGlyThrLeuAspGluSerValSerLeuAlaThr 237
 DB 838 ACTGGAATGGACGGTTATGACACACTGATGATGATGCTCTCCCTGCAAC 888
 RESULT 9
 BM557530 1019 bp mRNA linear EST 20-FEB-2002
 LOCUS BM557530 Homo sapiens cDNA clone IMAGE:5739935
 DEFINITION AGENCOURT_5563433 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5739935
 5', mRNA sequence.
 ACCESSION BM557530
 VERSION BM557530.1 GI:18799594
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1019)
 NIH-MGC http://mhc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LHM12734 Row: a Column: 24
 High quality sequence stop: 685.

FEATURES
 source
 1. 1019
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:573935"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_88"
 /note="Organ: small intestine; Vector: pCMV-Sport6;
 Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
 oligo-ct primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 256 a 254 c 236 g 271 t 2 others

ORIGIN

Alignment Scores:

Pred. No.: 4.64e-204 Length: 1019
 Score: 221.00 Matches: 221
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 63.14% Indels: 0
 DB: 12 Gaps: 0

US-09-745-506-37 (1-350) x BM557530 (1-1019)

QY 1 MetaspLeuYsAlaLeuSerSerLeuSnaSpheAlaSerLeuSerPheAlaGlu 20
 DB 107 ATGGATTGAAAGGCT 166
 QY 21 SerTrpAspaNValGlyLeuLeuValGluProSerProPheHisThrValAsnThrLeu 40
 DB 167 AGTGGGAGCATTGTTGGATTACTGCTGAGACCAAGCCACACACATACCTGAATACACTC 226
 QY 41 PheLeuThrAsnaSpLeuThrGluGluValMetGluValLeuGluLysAlaAsp 60
 DB 227 TTCTCTGACCAATGACTCTACTGAGAGAGTGTGAGGTGCTGCAAAAGGCAACAC 286
 QY 61 LeuLeuSerTrpHisProProLeuPheArgProMetLysArgIleThrTrpAsnThr 80
 DB 287 CTCATTCTCTCTACCATCCGCTATCTCTCCGACCCATGAAGCGCATTAACCTGGAAACACA 346
 QY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnATGValGlyIleTrpSerProHis 100
 DB 347 TGGAAAGAGCCGCTGTGTATCTCGGCGCTCGAAGAACAGATCGGATCTACTCTCTCAT 406
 QY 101 ThrAlaTrpAspaAlaAlaProGluGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
 DB 407 ACAGCGTATGATGTCGCCGCCAGGCGCTCAACAACATGTTGGCTAAAGGCTTGAGACT 466
 QY 121 CysTrpSerArgProIleHisProSerLysAlaProAsnTrpProThrGluGlyAsnHis 140
 DB 467 TGTACTCTCAGGCGCCATCATCTCTTCCAAAGCTCCCAACTCCCTACAGAGGAGAAACAC 526
 QY 141 ArgValGluPheAsnValAsnTrpThrGlnAspLeuAspLysValMetSerAlaValLys 160
 DB 527 CGAGTAGATTCACAGTTTACTACACCAAGACCTGGAGCAAAAGTATCTGTGCACTGAAA 586
 QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
 DB 587 GGAATTGACGGGTCTTGTCACTCTTTCTCTCTAGACCTGGTAATAGAGAACAAACA 646
 QY 181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200

DB 647 CGGATTATCTGAATTCTACTCAGAGGCTTTCATGTCAGGTGCTTCTTCCCG 706
 QY 201 AsnLysGlnLeuTrpGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHis 220
 DB 707 AACAAACACTTATATCAGAAAGACGAAATTCCTGCACTGAGAGAGCCTTGTCTTCTCAT 766

QY 221 Thr 221
 DB 767 ACT 769

RESULT 10
 AL529615

LOCUS 1201 bp mRNA linear EST 23-MAY-2003
 DEFINITION AL529615 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
 cDNA clone CS0DD006YH18 5-PRIME, mRNA sequence.

ACCESSION AL529615
 VERSION AL529615.2 GI:31067458
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12793108.

CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1287.f for more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DD006DD09QP1&cluster=1287.f>. Contact :
 Feng Liang Email: fliang@life.com URL: <http://fulllength.invitrogen.com/invitrogen>
 Faraday Avenue Genoscope sequence ID: CS0DD006DD09QP1.

FEATURES
 source

1. 1201

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DD006YH18"
 /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
 /clone_id="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 319 a 286 c 274 g 299 t 23 others

ORIGIN

Alignment Scores:

Pred. No.: 4.01e-199 Length: 1201
 Score: 216.00 Matches: 268
 Percent Similarity: 99.26% Conservative: 0
 Best Local Similarity: 99.26% Mismatches: 1
 Query Match: 61.71% Indels: 2
 DB: 9 Gaps: 0

US-09-745-506-37 (1-350) x AL529615 (1-1201)

QY 23 AspaNValGlyLeuLeuValGluProSerProPheHisThrValAsnThrLeuPheLeu 42
 DB 237 GACATGTTGGATTACTGTGTGAAACCAAGCCACACATCTGTAAATACACTCTCTCTG 296
 QY 43 ThrAsnaSpLeuThrGluGluValMetGluGluValLeuGlnLysAlaAspLeuIle 62
 DB 297 ACCAATGACCTGACGAGAGAGTGTGAGAGGTGTGCAAAAGAGCAGACCTCATY 356
 QY 63 LeuSerTrpHisProProIlePheArgProMetLysArgIleThrTrpAsnThrTrpLys 82


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|||||
Db 357 CTTCTCTACACCCGCTATCTCCGACCATGACGACATACCGAAGACATGAGG 416
Qy 83 GUAAGLeuVal11LeuArgAlaLeuGluAsnArgVal11GlySerProHisThrAla 102
Db 417 GAGCGCTGCTGTCGGGCTCTGGAGAACAGAGCTGATCTCTCTCATACAGCC 476
Qy 103 TTAAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaGlyLeuGlyVal11GlySerThr 122
Db 477 TATGATGCTGCGCCCGACGCGCTCAACAACTGGTGGCTTAAGGCTTGGAGCTTGATAC 536
Qy 123 SerArgProIleHisProSerIleAspAsnArgVal11GlySerProHisThrAla 142
Db 537 TCCAGGCCCATCATCTCTCCAAAGCTCCCACTACCTACACAGGAAACCCAGAT 596
Qy 143 GluPheAsnValAsnTrpThrGlnAspLeuAspVal11MetSerAlaVal11GlySer 162
Db 597 GAATTCACAGCTTAACACACCCAAAGCTGGACAAAGTCAATGCTCAGTGAAGAAGAT 656
Qy 163 AAspGlyValSerVal11ThrSerPheSerAlaArgThrGlyAsnGlnGlnGlnThrArg 182
Db 657 GACGGCTTCTGCTCCTCTCTTTCTGCTAGACCTGTAATAGAGAACACACGAT 716
Qy 183 AsnLeuAsnCysThrGlnGlnValAlaLeuMetGlnVal11AspPheLeuSerArgAsn 202
Db 717 AATCTGAATTTGACTCAGAAAGCTTGATGACAGCTGGTGAATTTCTTCCCGAACA 776
Qy 203 GlnLeuTrpGlnLeuThrGlnLeuLeuSerLeuGlnGlnProLeuLeuHisThrGly 222
Db 777 CAACCTTATCAGAAAGCGAAATCTGCTACGGAAGACCTTGGTCTTCTACATCTGGA 836
Qy 223 MetGlyArgLeuGlnCysThrLeuAspGlnSerVal11SerLeuAlaThrMetIle-AspArg 242
Db 837 ATGGGACGGTTATGACACTGATGATGATGCTCTCCCTGGCAACATGAG-TGATGAT 895
Qy 242 eIysArgHisLeuLeuSerHisIleArgLeuAlaLeuGlyVal11GlyArgThrLeu 262
Db 896 AAAAACAACACTTAACTATCTCATATTCGCTTACGCCCTGGGGGAGAACCTTACA 955
Qy 262 uSerGlnVal11Val11AlaLeuCysAlaGlySerGlySerVal11LeuGlnGly 282
Db 956 GTCTCAAGTCAAAAGTGTGGCCCTGTGTGGCTGTGGAGGAGGCTTGGAGGCTGT 1015
Qy 282 LgluAlaAspLeuTrpLeuThrGlyGlu 291
Db 1016 TGAGGCTGACCTTACTCAGAGGTGAG 1043

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RESULT 11
 BQ437698 877 bp mRNA linear EST 24-MAY-2002
 LOCUS AGENCOURT 7894666 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158334
 DEFINITION 5' mRNA sequence.
 ACCESSION BQ437698
 VERSION BQ437698.1 GI:21176774
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 877)
 NIH-MGC <http://mgi.ncl.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLN at:
<http://image.llnl.gov>
 Plate: LHAM13505 row: k column: 07

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FEATURES             High quality sequence stop: 667.
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                    /clone="IMAGE:6158334"
                    /issue_type="melanotic melanoma"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_72"
                    /note="Organ: skin; Vector: pCMV-Sport6; site_1: NotI;
                    site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
                    Average insert size 2 kb. Library constructed by life
                    Technologies."
BASE COUNT          247 a 181 c 206 g 242 t 1 others
ORIGIN
Alignment Scores:
Pred. No.:          2,51e-197          Length:      877
Score:              214.00             Matches:      214
Percent Similarity: 100.00%            Conservative: 0
Best Local Similarity: 100.00%          Mismatches:  0
Query Match:        61.14%              Indels:      0
DB:                  13                  Gaps:        0
US-09-745-506-37 (1-350) x BQ437698 (1-877)
Qy 137 GUGGlyAsnHisArgVal11GluPheAsnValAsnTrpThrGlnAspLeuAspVal11Met 156
Db 26 GAGGGAACACACGAGAGTGAATTCACGTTAACTACACCCAAAGCTGGACAAAGTCATG 85
Qy 157 SerAlaVal11GlyGlyLeuAspGlyVal11SerVal11ThrSerPheSerAlaArgThrGly 176
Db 86 TCTGCACTGAAGAAATGACGCTGTTCTGCTACTTCTTTCTGCTAGAGATCGTAAT 145
Qy 177 GUGGlnGlnThrArgGlyLeuAsnLeuAsnCysThrGlnGlnAlaLeuMetGlnVal11Asp 196
Db 146 GAGGAACAAACACGAGATTAATTCGAATTTGACTACAGAAAGCTTGAATGACGAGTGAAT 205
Qy 197 PheLeuSerArgAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 216
Db 206 TTTCTTCCCGGAACAAACCTTATTCACAAACGGAATTTGCTACTGGAAGAGCT 265
Qy 217 LeuLeuLeuHisThrGlyMetGlyArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 236
Db 266 TTGCTTCTACATCTGGAATGAGGACGCTTATGCACACTGATGATGCTCTCCCTGGCA 325
Qy 237 ThrMetIleAspArgGlyLeuArgHisLeuLeuSerHisIleArgLeuAlaLeuGly 256
Db 326 ACCATGATGATGAATTAACAAACACCTTAACTATCTCATATTCGCTTACGCCCTTGGG 385
Qy 257 ValGlyArgThrLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 276
Db 386 GTGGGGAACCTTGAAGTCTCAAGTCAAGTGTGGCCCTGTGTGCTGTGCTGTGGAGC 445
Qy 277 SerVal11LeuGlnGlyVal11GluAlaAspLeuTrpLeuThrGlyGlnMetSerHisAsp 296
Db 446 AGCGTTCTGAGAGGTGTGAGGCTGACCTTACTCTACAGATGATGATGATGATGATGAT 505
Qy 297 ThrLeuAspAlaAsnGlnGlyLeuAsnVal11LeuGlnGlnGlnGlnGlnGlnGlnGln 316
Db 506 ACTTTGATGCTCTCTCCCAAGGAATTAAGTATCTCTCTGTAACACACCAACACTGAA 565
Qy 317 ArgGlyPheLeuSerAspLeuArgAspMetLeuAspSerHisIleGlnGlnGlnGlnGln 336
Db 566 CGAGGCTTCTTCTGCTGCTTCAAGATATCTGATTTCTGAGATTAAGATTAAT 625
Qy 337 IleIleLeuSerGlnTrpAspArgAspProLeuGlnVal11 350
Db 626 ATTATCTATCAGAGACTGACAGGAGACCTCTTCAAGTGTGTA 667

```

RESULT 12
 B0859307

/note="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 191 a 196 c 173 g 198 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 2,02e-196 Length: 759
 Score: 213.00 Matches: 213
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60,868 Indels: 0
 DB: 10 Gaps: 0

US-09-745-506-37 (1-350) x BE275324 (1-759)

OY 1 MetAspLeuLysAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 DB 86 ATGGATTGAAGGCTCTCTCTCTCTGAAATGACTTGCATCCCTCGTTGCTGAG 145
 OY 21 SerTPAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
 DB 146 ACTTGAGACATGTTGATTACTGCTGGAACCAAGCCACACATCTGTAATTAACACTC 205
 OY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
 DB 206 TTCCTGACCAATGACTGACTGAGGAATGATGAGAGAGTGTCTGCAAAAGAGGAGAGC 265
 OY 61 LeuIleLeuSerThrHisProProIlePheArgProMetLysArgIleThrTPAsnThr 80
 DB 266 CTCATTCTCTCTACCATCGCTATCTCCGACCATGAAGCGATTAACCTGGAAACA 325
 OY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
 DB 326 TGAAGAGACGCGCTGATCCGGGCTCGGAGAAAGAGTGGTATCTACTCTCAT 385
 OY 101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
 DB 386 ACAGCCTATGATGCTGCGCCCGGCGCTCAACATGTTGGCTTAAGGCTTGGAGCT 445
 OY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
 DB 446 TGTACCTCCAGGCGCATACATCTTCCAAAGCTCCCACTACCTACAGAGGAAACAC 505
 OY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
 DB 506 CGAGTGAATTCACACTTAACATACACCAAGACCTGGACAAAGTCTGTCTGAGTGA 565
 OY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
 DB 566 GGAATGAGCGTGTCTCTCACTCTTTCTTCTGTAAGACCTGTAATGAGAAACA 625
 OY 181 ArgIleAsnLeuAsnLysThrGlnLysAlaLeuMetGluValValAspPheLeuSerArg 200
 DB 626 CGGATTAATCTGAATGTACTCAGAAAGGCTTGATCAGGTGATATTCTTCCCG 685
 OY 201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeu 213
 DB 686 AACAAACACATTATCAGAAAGGAAATTCGTCTACTG 724

RESULT 14
 LOCUS B1755123 817 bp mRNA linear EST 25-SEP-2001
 DEFINITION 60302837F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5193320 5',
 mRNA sequence.
 ACCESSION B1755123
 VERSION B1755123.1 GI:15746701
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 817)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsd-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLNL1483 row: j column: 09
 High quality sequence start: 3
 Location/Qualifiers

FEATURES
 source
 1. 817
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5193320"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_114"
 /note="Organ: brain; Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb. Insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC Library."

BASE COUNT 205 a 211 c 183 g 218 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.92e-194 Length: 817
 Score: 211.00 Matches: 224
 Percent Similarity: 99.56% Conservative: 0
 Best Local Similarity: 99.56% Mismatches: 0
 Query Match: 60,29% Indels: 1
 DB: 12 Gaps: 0

US-09-745-506-37 (1-350) x B1755123 (1-817)

OY 1 MetAspLeuLysAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 DB 109 ATGGATTGAAGGCTCTCTCTCTCTGAAATGACTTGCATCCCTCGTTGCTGAG 168
 OY 21 SerTPAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
 DB 169 AGTTGGACAAATTTGGATTACTGCTGGAACCAAGCCACACATCTGTAATTAACACTC 228
 OY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
 DB 229 TTCCTGACCAATGACTGACTGAGGAATGATGAGAGAGTGTCTGCAAAAGAGGAGAC 288
 OY 61 LeuIleLeuSerThrHisProProIlePheArgProMetLysArgIleThrTPAsnThr 80
 DB 289 CTCATTCTCTCCATACATCGCTATCTCCGACCATGAAGCGCATTAACCTGGAACACA 348
 OY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
 DB 349 TGAAGAGCGCGCTGATCCGGGCTCTGGAACAAGACTCGGTATCTACTCTCAT 408
 OY 101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
 DB 409 ACAGCCTATGATGCTGCGCCCGGCGCTCAACATCTGTTGGCTTAAGGCTTGGAGCT 468

QY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
DB 469 TGTACCTCCAGGCCCATCATCTCTCCAAAGCTCCCAACTACCTACAGAGGAACAC 528
QY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
DB 529 CGACTAGAAATTCACAGTTACTACACCCAGACCTGGCAAAAGTCATGTCTGCAGTGA 588
QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluThr 180
DB 589 GGAATTGACGGTGTCTTCTGACTCTTTTCTGCTAGGACTGGTAATGAGAAACA 648
QY 181 ArgIle-AsnLeuAsnCysThrGlnLysAlaLeuMetGlnValAlaAspPheLeuSer 200
DB 649 CGGATTTAATCTGAATGTACTACAGAAAGCTTGTGACAGGTGGTAATTTCTTCCCG 708
QY 200 GAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHis 220
DB 709 GAAACAACAACTTATCATGAGAGGAAATCTGTCACTGAGAGAAAGCTTGTCTTCA 768
QY 220 sThrGlyMetGly 224
DB 769 TACTGGAATGGCA 781

RESULT 15
BX377118/c 1201 bp mRNA linear EST 08-MAY-2003
LOCUS BX377118 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1002YM20 3-PRIME, mRNA sequence.
ACCESSION BX377118
VERSION BX377118.1 GI:30448573

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1002BG10NP1&cluster=1287.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1002BG10NP1.

FEATURES
source
Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1002YM20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 319 a 250 c 257 g 325 t 50 others
ORIGIN

Alignment Scores:
Pred. No.: 2.72e-193 Length: 1201
Score: 210.00 Matches: 223
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 0

Query Match: 60.00% Indels: 1
DB: 13 Gaps: 0
US-09-745-506-37 (1-350) x BX377118 (1-1201)

QY 125 ProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHisArgValGluPhe 144
DB 913 CCCATACATCCCTTCCAAAGCTCCCAACTACCTACAGAGGGAACCAACCGATGAAATTC 854
QY 145 AsnValAsnTyrThrGln-AspLeuAspLysValMetSerAlaValLysGlyIleAspGly 164
DB 853 AACCTTAATCTACACCAAGACCTGGACAAAGTCATGTCTGCACTGAAGAATGACGG 794
QY 164 ValSerValThrSerPheSerAlaArgThrGlyAsnGluGluThrArgIleAsnLe 184
DB 793 TGTTCGTGCTCACTCTTTTCTGCTAGAACTGTAATGAGGAACAAACACGGAATTAATCT 734
QY 184 uAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLysGluLe 204
DB 733 GAAATGTACTAGAAAGCTTGTGATGACAGGTGTGATATTTCTTCCCGAACAACAATCT 674
QY 204 uTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHisThrGlyMetGly 224
DB 673 TTATCAGAAAGACGGAATTTCTGTCACTGAGAGACCTTGTCTTACATACTGGAATGG 614
QY 224 ValGluCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIleLysArg 244
DB 613 ACGTTATGACACACTGATGATCTGTCTCCCTGCAACATGATGATGATGATGATGATG 554
QY 244 GHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGluSerGly 264
DB 553 ACACCTAAACTATCTCATTTCTGCTTATGCTTGGGGTGGGGAACCTTAGAGTCTCA 494
QY 264 nValLysValAlaLeuCysAlaGlySerGlySerSerValLeuGlnGlyValGluAl 284
DB 493 AGTCAAATCTCGTGGCCCTGTGCTGTGCTGCGGAGCGCTTCTGCGAGGGTGTGAGGC 434
QY 284 aAspLeuTyrLeuThrGlyGluMetSerHisAspThrLeuAspAlaLeuSerGlnGly 304
DB 433 TGACCTTAACTCACAGGTGAGATGTCACATCATGATACTTTGGATGCTGCTTCCAAAG 374
QY 304 yIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeuSerAspLeuArg 324
DB 373 AATAAATCTATCCCTGTGTAACACAGACACAGACGAGGCTTTCTTCTGACCTTGC 314
QY 324 gAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSerGluTyrAspArg 344
DB 313 AGATATGCTGATTTCTCTCACTTGAGAAATGATTAATATTAATCTATCAGAGACTGACAG 254
QY 344 gAspProLeu 347
DB 253 GGACCTCTN 244

Search completed: August 23, 2003, 22:13:46
Job time : 1904 secs